ORIGIN

Query Match   89.5%;   Score 1264; DB 20;   Length 1269;
Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches 1266; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      2 ATGAGGAGAAAATAATGATGATCAAAAGGAAGAAGGAGGAGGAGGTGTTCGTGCTTGTCTGCCAA 61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77 ATGAGGAGAAAATAATGATGATCAAAAGGAAGAAGGAGGAGGAGGTGTTCGTGCTTGTCTGCCAA 136

Qy     62 CTGTAATGGTTGTTGTTTGGGAATACATCAACAGCCCAGAAGGTTCTTTGTTCTGGGATAT 121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137 CTGTAATGGTTGTTGTTTGGGAATACATCAACAGCCCAGAAGGTTCTTTGTTCTGGGATAT 196

Qy    122 ACCAGTCAAAAAACCCAGAAGTTGGCAGCAGTGCTCAGAGGGCTGGTTCGGAGCT 181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 ACCAGTCAAAAAACCCAGAAGTTGGCAGCAGTGCTCAGAGGGCTGGTTCGGAGCT 256

Qy    182 GGGTTTAACAATGGGACTCACAGTTACCACGAAGAAGAAGAAGAAAGG 241
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 AACAAAGAAAAGAAAGACAACAGAGGAGAGCTTCCGCTTAATCCTGAGA 301

Qy    242 AACAAAGAAAAGAAAGACAACAGAGGAGAGCTTCCGCTTAATCCTGAGA 301
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 AACAAAGAAAAGAAAGACAACAGAGGAGAGCTTCCGCTTAATCCTGAGA 376

Qy    302 AACGCCCAGAGGTCGTGACCATAACCAGATGGGAAGGGCTTCCAGTGGTATGGGAAGGCACTT 361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 AACGCCCAGAGGTCGTGACCATAACCAGATGGGAAGGGCTTCCAGTGGTATGGGAAGGCACTT 436

Qy    362 ACAACAGAGCCGTCTTAGATAATTATTTATTAATGCAAAACAGAAAAATTACCGTGGGCTTGACGG 421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 ACAACAGAGCCGTCTTAGATAATTATTTATTAATGCAAAACAGAAAAATTACCGTGGGCTTGACGG 496

Qy    422 TTTTTGCTGTCGGAAGATACATTGAGCAATTACTTGGAGGAGTTCTTTAATACTGCAAATA 481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497 TTTTTGCTGTCGGAAGATACATTGAGCAATTACTTGGAGGAGTTCTTTAATACTGCAAATA 556

Qy    482 CATACTTCATGGTTGGCCACAAAAGTCATCTTTTACATCATTGGGTGGATGATAATCTCCAGGA 541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 CATACTTCATGGTTGGCCACAAAAGTCATCTTTTACATCATTGGGTGGATGATAATCTCCAGGA 616

Qy    542 TGCCTTTGATAGAGCTGTGGGTCCTCTCGCGTTCCTTTAAAGTGTTTGAGATCAAGTCCGAGA 601
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 TGCCTTTGATAGAGCTGTGGGTCCTCTCGCGTTCCTTTAAAGTGTTTGAGATCAAGTCCGAGA 676

Qy    602 AGAGGTGGCAAGACAATCAGCATGATCGCGCAATGAAGACCATCCGGGGAGCACAATCCTGGCC 661
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 AGAGGTGGCAAGACAATCAGCATGATCGCGCAATGAAGACCATCCGGGGAGCACAATCCTGGCC 736

Qy    662 ACATCCAGCACGAGGTGGACTTCCTCTTCTCGCGTTGGGACGTGGGACTCAGGTCTTCAAAACA 721
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 ACATCCAGCACGAGGTGGACTTCCTCTTCTCGCGTTGGGACGTGGGACTCAGGTCTTCAAAACA 796

Qy    722 ACTTTGGGGTGGAGACCCTGGGCGACTCGGGGCTCAGCCTGGTCTGGTTACAAGG 781
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    797 ACTTTGGGGTGGAGACCCTGGGCGACTCGGGGCTCAGCCTGGTCTGGTTACAAGG 856

Qy    782 CACATCCCTGACGAGTTCACCTACGAGAGGCGGAAGGAGTCCGCAGCCTACATTCCGTTTG 841
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    857 CACATCCCTGACGAGTTCACCTACGAGAGGCGGAAGGAGTCCGCAGCCTACATTCCGTTTG 916

Qy    842 GCCAGGGGGGATTTTATTACCACGCACCACCATTTTTGGGGAACAACCACTCAGGTTCTAA 901
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    917 GCCAGGGGGGATTTTATTACCACGCACCACCATTTTTGGGGAACAACCACTCAGGTTCTAA 976

Qy    902 ACATCACTCAGGAGTGCTTCAAGGGAATCCTCCAGGACAAGAAAATGACATAGAAGCCG 961
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    977 ACATCACTCAGGAGTGCTTCAAGGGAATCCTCCAGGACAAGAAAATGACATAGAAGCCG 1036

Qy    962 AGTGGCATGATGAAAAGCCAATCTAAACAAGTATTTCCTTCTCAACAAACCACTAAAATCT 1021
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037 AGTGGCATGATGAAAAGCCAATCTAAACAAGTATTTCCTTCTCAACAAACCACTAAAATCT 1096
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Db   1022 TATCCCCAGAATACTGCTGGGATTATCACAATAGGCAGTGTCTGTTGGATATTAGGATTGTCA 1081
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1097 TATCCCCAGAATACTGCTGGGATTATCACAATAGGCAGTGTCTGTTGGATATTAGGATTGTCA 1156

Db   1082 AGATAGCTTGGCCAGAAAAAAGAGTATAATTTGGTTAGAAATAAGGCATGTCTGTGGAATTAAAATTG 1141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1157 AGATAGCTTGGCCAGAAAAAAGAGTATAATTTGGTTAGAAATAAGGCATGTCTGTGGAATTAAAATTG 1216

Db   1142 TGCCAGCAGTTTTCTCGAATTTGAAAGAGTATTACTCTGGCTACTTCTCCAGAGAAGTAGC 1201
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1217 TGCCAGCAGTTTTCTCGAATTTGAAAGAGTATTACTCTGGCTACTTCTCCAGAGAAGTAGC 1276

Db   1202 ACTTAATTTAAACTTTTATAAAAAATACTAACAAAATACCAACACAGTAAGTACATATTAT 1261
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1277 ACTTAATTTAAACTTTTATAAAAAATACTAACAAAATACCAACACAGTAGTACATATTAT 1335

Db   1262 TCTTCCTT 1269
            ||||||||
Qy   1337 TCTTCCTT 1344
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RESULT 2

LOCUS   PIGA13G   1343 bp   mRNA   MAM   03-JAN-1995
DEFINITION   Sus scrofa (clone pPGT-3) alpha 1,3-galactosyltransferase mRNA,
             complete cds.
ACCESSION   L36535
NID   g609566
KEYWORDS   alpha-1,3-galactosyltransferase.
SOURCE   Sus scrofa spleen and liver cDNA to mRNA.
  ORGANISM   Sus scrofa
             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
             Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 1343)
  AUTHORS   Sandrin,M.S., Dabkowski,P.L., Henning,M.M., Mouhtouris,E. and
             McKenzie,I.F.C.
  TITLE   Characterization of cDNA clones for porcine a(1,3)galactosyl
             transferase: The enzyme generating the Gala(1,3)Gal epitope
             Xenotransplantation (1994) In press
  JOURNAL   Location/Qualifiers
FEATURES   source   1..1343
                             /organism="Sus scrofa"
                             /note="(vector lambda gt10) (vector lambda gt11)"
                             /db_xref="taxon:9823"
                             /clone="pPGT-3"
             5'UTR   /tissue_type="spleen and liver"
             mRNA   1..1343
             CDS   1..49
                             50..1129
                             /codon_start=1
                             /product="alpha-1,3-galactosyltransferase"
                             /db_xref="PID:g609567"
                             /translation="MNVKGRVVLSMLLVSTVMVFWEYINRNPEVGSSAQRGWFPSW
                             FNNGRHSYHEEEDAIGNEKEQRKEDNRGELPLVDWFNPKEPEVVTITRWKAPVVNEG
                             TYNRAVLDNYIYAKQMITVGLTVPAVGRVIEHILEEFLLSANTFMVGHKVIFYIMVDD
                             ISRMPLIELGPLRSFKVFEIKSERKWQDISMRMKTIGEHILAHIQHEVDFLFCIDVD
                             QVFQNNFGVEGLGSVAQLQAWWYTAHPDEFTYERRKESAAYIPFGQGDFYYHAAIFG
                             GTPTQVLNIIQECFKGILQDKENDIEAEWHDESHLNKYFLLNKPTKILSPEYCWDYHI
                             GMSVDIRIVKIAWQKKEYNLVRNNI"
             3'UTR   1130..1343
BASE COUNT   399 a   281 c   324 g   339 t
ORIGIN

Query Match   84.6%;   Score 1195; DB 20;   Length 1343;
Best Local Similarity 98.9%;   Pred. No. 0.00e+00;
Matches 1214; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Db    108 TGTTTTGGGAATACATCAACAGAAAACCCAGAAGTTGGCAGCAGTTGGCAGCGTTCAGGGGGGCTGGT 167
            ||||  ||| |   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    185 TGTTCTGGATATACCAGTCAAAAAACCCAGAAGTTGGCAGCAGTTGGCAGCGTTCAGGGGGGCTGGT 244

Db    168 GGTTTCCGAGCTGGTTTAACAATGGGACTCACAGTTACCACGAAGAAGAAGACGCTATAG 227
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1307 TAATCAGATGTAAATCCCAATGATTTC 1334
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Qy  1385 TAATCAGATGTAAATCCCAGTGATTTC 1412
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Qy   245 GGTTCCAGCTCGTTTAACAATGGSACTCACAGTTACCACGAAGAAGACGCTATAG 304
Db   228 GCAACGAAAAGGAACAAAGAAGAAGACAACAGAGGAGGAGGAGAAGACGAAGAAGAGA 287

Qy   305 GCAACGAAAAGGAACAAAGAAGAAGACAACAGAGGAGGAGGAG 364
Db   288 TTAATCCTGAGAAACGCCCAGAGAGGTCGTGACCATAACCAGTAGTGGAGTGGTAT 347

Qy   365 TTAATCCTGAGAAACGCCCAGAGAGGTCGTGACCATAACCAGTAGTGGAGTGGTAT 424
Db   348 GGGAAGGCACTTACAACAGAGACCGTCTTAGATAGTTAATTATTATGCCAAACAGAAAATTACCG 407

Qy   425 GGGAAGGCACTTACAACAGAGACCGTCTTAGATAGTTAATTATTATGCCAAACAGAAAATTACCG 484
Db   408 TGGGCTTGACGGTTTTGCTGTCGGAAGATACATTGAGCAATACTTGGAGGAGTTCTTAA 467

Qy   485 ATAATCTCAGGAGATGCCTTTGATAGAGTGTGGGGTCCTCTTGCGTTCCTTTACATCATGGTGGATG 544
Db   468 TATCTGCAAATACATACTTCATGGTTGGCCACAAAGTCATCTTTACATCATGGTGGATG 527

Qy   545 TATCTGCAAATACATACTTCATGGTTGGCCACAAAGTCATCTTTACATCATGGTGGATG 604
Db   528 AIAATCTCAGGAGATGCCTTTGATAGAGTGTGGGGTCCTCTTGCGTTCCTTTAAGTGTTTGAGA 587

Qy   588 TCAAGTCCGAGAAGGAGGTGGCAAGACAATCAGCATGATGAGTGAAGAACCAATCGGGGAGC 647
Db   505 ATAATCTCAGGAGATGCCTTTGATAGAGCGTGGGGTCCTCTTGCGTTCCTTTAAAGTGTTTGAA 564

Qy   588 TCAAGTCCGAGAAGGAGGTGGCAAGACAATCAGCATGATGAGTGAAGAACCAATCGGGGAGC 647
Db   545 TATCTGCAAATACATACTTCATGGTTGGCCACAAAGTCATCTTTACATCATGGTGGATG 604

Qy   648 ACATCTCGGCCACATCCAGCACCAGGTGGACACTTCCTCTTCTCGCAATTGACCTGGATCAGG 707
Db   565 TCAAGTCCGAGAAGGAGGTGGCAAGACAATCAGCATGATGAGTGAAGAACCAATCGGGGAGC 624

Qy   648 ACATCTCGGCCACATCCAGCACCAGGTGGACACTTCCTCTTCTCGCAATTGACCTGGATCAGG 707
Db   725 ACATCCTGGCCAATCATGAAAAGCCTACTAAACAAGTAGTTCCTTCTCCTTCAACAAAC 784

Qy   708 TCTTCCAAACAACTTTGGGGTGGAGACCCTGGGCCCAGTCGTTCAGTGTTACAGGCCT 767
Db   708 TCTTCCAAACAACTTTGGGGTGGAGACCCTGGGCCCAGTCGTTCAGTGTTACAGGCCT 767

Qy   768 GGIGGTACAAGGCACATCCTGACGAGTTCACTTACGAGAGGGGGAAGGAGTCCGCAGCCT 827
Db   785 TCTTCCAAACAACTTTGGGGTGGAGACCCTGGGCCCAGTCGTTCAGTGTTACAGGCCT 844

Qy   845 GGIGGTACAAGGCACATCCTGACGAGTTCACTTACGAGAGGGGGAAGGAGTCCGCAGCCT 904
Db   768 GGIGGTACAAGGCACATCCTGACGAGTTCACTTACGAGAGGGGGAAGGAGTCCGCAGCCT 827

Qy   905 ACATTCCGTTTGGGCCAGGGGATTTTTATTACCACGCACCCATTTTTGGGGAACACCA 964
Db   828 ACATTCCGTTTGGGCCAGGGGATTTTTATTACCACGCACCCATTTTTGGGGAACACCA 887

Qy   965 CTCAGGTTCTAAACATCACTCAGGAGTGCTTCAAGGGAATCCTCCAGGACAAGGAAAAATG 1024
Db   888 CTCAGGTTCTAAACATCACTCAGGAGTGCTTCAAGGGAATCCTCCAGGACAAGGAAAAATG 947

Qy  1025 ACATAGAAGCCGAGTGGCATGAGAGCCATCTAAACAAGTAGTTCCTTCTCCTTCAACAAAC 1084
Db   948 ACATAGAAGCCGAGTGGCATGAGAGCCATCTAAACAAGTAGTTCCTTCTCCTTCAACAAAC 1007

Qy  1085 CCACTAAAATCTTATCCCAGAATAGTCGTGGGATAATACTGCTGCAGCAATGTCGTGTGGATA 1144
Db  1008 CCACTAAAATCTTATCCCAGAATAGTCGTGGGATAATACTGCTGCAGCAATGTCGTGTGGATA 1067

Qy  1145 TTAGGATTGTCAAGAATAGCTTGGCCAGAAAAAAAGAGTATAATTAATTTGGTTAGAAATAACATCT 1204
Db  1068 TTAGGATTGTCAAGAATAGCTTGGCCAGAAAAAAAGAGTATAATTAATTTGGTTAGAAATAACATCT 1127

Qy  1205 GACTTTAAATTGTCCCACACAGTTTTCTGAATTGAAAGAGTATTACTCTGGCTACTTCCT 1264
Db  1128 GACTTTAAATTGTCCCACACAGTTTTCTGAATTGAAAGAGTATTACTCTGGCTACTTCCT 1187

Qy  1265 CAGAGAAGTAGCACTTAATTTAACTTTTAAAAAATAACAAAATACCAACACAGTA 1324
Db  1188 CAGAGAAGTAGCACTTAATTTAACTTTTAAAAAATAACAAAATACCAACACAGTA 1246

Qy  1247 ACTACATATTATCTTCCTTGCAACTTTGAGCCTTGTCAAATGGGAGAATGACTCTGTAG 1306
Db  1205 GAGGGGCTGGTGGTTCCGAGCTGGGTTTAACAATGGGACTCACAGTTACCACGAAGAAGA 1264
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RESULT 3

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LOCUS       BOVGSTA       1828 bp    mRNA            MAM       15-DEC-1989
DEFINITION  Bovine alpha 1,3 galactosyltransferase mRNA completed cds.
ACCESSION   J04989
NID         g163123
KEYWORDS    alpha-1,3-galactosyltransferase.
SOURCE      Bovine thymus, cDNA to mRNA, clone 31A.
  ORGANISM  Bos taurus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1828)
  AUTHORS   Joziasse,D.H., Shaper,J.H., Van den Eijnden,D.H., Van Tunen,A.J.,
            and Shaper,N.L.
  TITLE     Bovine alpha 1-3-galactosyltransferase: Isolation and
            characterization of a cDNA clone: Identification of homologous
            sequences in human genomic DNA
  JOURNAL   J. Biol. Chem. 264, 14290-14297 (1989)
  MEDLINE   89340543
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by D.H.Joziasse, 15-AUG-1989.
FEATURES             Location/Qualifiers
     source          1..1828
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
     mRNA            <1..1828
                     /note="GSTA mRNA (alt.)"
     mRNA            <1..1655
                     /note="GSTA mRNA (alt.)"
     CDS             469..1575
                     /note="alpha 1-3 galactosyltransferase"
                     /codon_start=1
                     /db_xref="PID:g163124"
                     /translation="MNVKGKVILLMLVVSTVIVVFWEYIHSPEGSLFWINPSRNPEVG
                     GSSICKSWWLPFMFNNSYHEEDGDINEEFPQPNEDESKLSDWNPFFPPEVVTMTK
                     WKAPVVWEGTYNRAVLDNYYAKQRITVGLTVFAVGRYIEHYLEEFLTSANKHFWGHP
                     VIFYIMVDDVSRMPLIELGPLRSFKVIKPEKRWQDISMMRMKTIGEHIVAHIQHEV
                     DFLFCMDVDQVFQDKFGVETLGESVAQLQANWYKADPNDFTYERRKESAAYIPFGEGD
                     FYYHAAIFGGTPTQVLNITQECFKGILKDKNDIEAQWHDESHLNKYFLLNKPTKIL
                     PEICWDYHIGLPADIKLVKMSWQTKEYNVVRNNV"
BASE COUNT        493 a    450 c    479 g    406 t
ORIGIN      144 bp upstream of BglI site.
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Query Match   67.6%;   Score 955;   DB 20;   Length 1828;
Best Local Similarity 87.9%;   Pred. No. 0.00e+00;
Matches 1247;   Conservative 0;   Mismatches 148;   Indels 24;   Gaps 15;

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Db   375 AGCCCTCGCCTCCTTCTGCAGAACGGAGCTCAGTAGAACCTGGTACTTTTGCCTTTACTC 434
         |||||||||||||||||||||| | ||||||||||| ||||   ||||||||||||||||
Qy     1 AGCCCTGGCCTCCTTCTGCAGAACGGAGCTCACTAGAACTTG----TTTCGCCTTTACTC 56

Db   435 TAGGAGGAGGAGAAGAGACGATGAGGAGAAGAAAAATGAATGTCAAAAGGAGAGAATTCT 494
         |||||||||||||||| || |||||||||||||| |||||||||||||||||||||||||
Qy    57 TGGGGGGAGGAGAAGCAGAGGATGAGGAGAGAGAGCAGCTCACTAGAACTG---------- 116

Db   495 GTCAATGCTGGTTGTCTCAACTGTCATGTGTGTTGTGTTTGGGAATATATTCCACAGCCCAGA 554
         ||| |||||| ||| |||| |||||||||| | ||||||| ||||||||||||| |||||||
Qy   117 GTCAATGCTGCTTGTCTCAACTGTTAATGTTGTGTTTGGGAATAACATCAAACAGGCCCAGA 176

Db   555 AGGCTCTTGTTCTGGATCTCAACTGTCAATGTTGTGTTGTGTTTGGGAATATATTCCACAGCCCAGA 614
         ||||||||||||| || |||||||||||||||||||||||||||||||| |||||||||||
Qy   177 AGGTTCTTGTTCTGGATATACCAGTCAAAAAAACCCAGAAGTTGGGAATACCAGCCAGA 233

Db   615 GAAGGGGCTGGTGGTTCCGAGCTGGGTTTAACAATGGGACTCACAGTTACCACGAAGAAGA 668
         || ||||||| ||||| |||||||||||| |||||||||||| | |||||||||||||||
Qy   234 GAGGGGCTGGTGGTTCCGAGCTGGGTTTAACAATGGGACTCACAGTTACCACGAAGAAGA 293
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RESULT   2
ID   US-08-378-617-7 STANDARD; DNA; UNC; 1412 BP.
AC   XXXXXX
DE   Sequence 7, Application US/08378617
DT   Sequence 7, Application US/08378617
     GENERAL INFORMATION:
XX   APPLICANT: d'Apice, Anthony J.F.
XX   APPLICANT: Pearse, Martin J.
XX   APPLICANT: Robins, Allan J.
XX   APPLICANT: Crawford, Robert J.
XX   APPLICANT: Rathjen, Peter D.
XX   TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF
XX   TITLE OF INVENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION
XX   NUMBER OF SEQUENCES: 33
XX   CORRESPONDENCE ADDRESS:
XX   ADDRESSEE: Fish & Richardson
XX   STREET: 120 South Sixth Street, Suite 2500
XX   CITY: Minneapolis
XX   STATE: MN
XX   COUNTRY: USA
XX   ZIP: 55402
XX   COMPUTER READABLE FORM:
XX   MEDIUM TYPE: Floppy disk
XX   COMPUTER: IBM PC compatible
XX   OPERATING SYSTEM: PC-DOS/MS-DOS
XX   SOFTWARE: PatentIn Release #1.0, Version #1.30B
XX   CURRENT APPLICATION DATA:
XX   APPLICATION NUMBER: US/08/378,617
XX   FILING DATE: 25-JAN-1995
XX   CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
    NAME: Ellinger, Mark S.
    REGISTRATION NUMBER: 34,812
    REFERENCE/DOCKET NUMBER: 06868.0050U1
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (612) 925-5600
    TELEFAX: (612) 288-9696
INFORMATION FOR SEQ ID NO: 7.
SEQUENCE CHARACTERISTICS:
    LENGTH: 1412 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: DNA

SEQUENCE: 1412 BP; 288 A; 422 C; 344 G; 358 T; 0 OTHER.

Query Match   99.58%; Score 1406; DB 30; Length 1412;
Best Local Similarity 99.58%;
Matches 1409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT   3
ID   US-08-188-607B-7 STANDARD; DNA; UNC; 1412 BP.
AC   xxxxxx
DT
DE   Sequence 7, Application US/08188607B
     Sequence 7, Application US/08188607B
GENERAL INFORMATION:
    APPLICANT: d'Apice, Anthony J.F.
    APPLICANT: Pearse, Martin J.
    APPLICANT: Robins, Allan J.
    APPLICANT: Crawford, Robert J.
    APPLICANT: Rathjen, Peter D.
    TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF HYPERACUTE
    NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Patterson & Keough, P.A.
    STREET: 527 Marquette Avenue South
    CITY: Minneapolis
    STATE: Minnesota
    COUNTRY: USA
    ZIP: 55402
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: Apple Macintosh
    OPERATING SYSTEM: Macintosh System 7.0
    SOFTWARE: Macintosh Text File
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08,188,607B
    FILING DATE: 27-01-1994

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CC   CLASSIFICATION: 424
CC   PRIOR APPLICATION DATA:
CC   APPLICATION NUMBER:
CC   FILING DATE:
CC   ATTORNEY/AGENT INFORMATION:
CC     NAME: Mark S. Ellinger
CC     REGISTRATION NUMBER: 34,812
CC     REFERENCE/DOCKET NUMBER: 1175.04-US-01
CC   TELECOMMUNICATION INFORMATION:
CC     TELEPHONE: 612/349-5740
CC     TELEFAX: 612/349-9266
CC   INFORMATION FOR SEQ ID NO: 7:
CC   SEQUENCE CHARACTERISTICS:
CC     LENGTH: 1412
CC     TYPE: nucleic acid
CC     STRANDEDNESS: double stranded
CC     TOPOLOGY: linear
CC   MOLECULE TYPE: cDNA
CC   DESCRIPTION:
CC   HYPOTHETICAL: no
CC   ANTI-SENSE: no
CC   ORIGINAL SOURCE:
CC     ORGANISM: Sus scrofa
CC     STRAIN:
CC     INDIVIDUAL ISOLATE:
CC   IMMEDIATE SOURCE:
CC     LIBRARY:
CC     CLONE:
CC   POSITION IN GENOME:
CC     CHROMOSOME/SEGMENT:
CC   FEATURE:
CC     NAME/KEY: Porcine alpha 1,3-Galt cDNA sequence derived from overlapping pc
CC   PUBLICATION INFORMATION:
CC     AUTHORS:
CC     TITLE:
CC     JOURNAL:
CC     VOLUME:
CC     ISSUE:
CC     PAGES:
CC     DATE:
SQ   SEQUENCE 1412 BP; 422 A; 288 C; 344 G; 358 T; 0 OTHER.
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Query Match          99.6%;  Score 1406;  DB 25;  Length 1412;
Best Local Similarity 99.8%;  Pred. No. 0.00e+00;
Matches 1409;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;
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Qy    361 TGGTTTAATCCTGAGAAAGCCCAGAGGTCGTCGACCATAACC!

Db      1 AGCCCTGCCTCCTTCCTGCAGAGCAGAGCTCACTAGAACTTGTTTCGCCTTTACTCTGGG   60
          |||||||||||||||||||||||| |||||||||||||||||||||||| |||||||||||
Qy      1 AGCCCTGCCTCCTTCCTGCAGAGAGAGCTCACTAGAACTTGTTTCGCTTTTACTCTGGG    60

Db     61 GGGAGAAGAAGCAGAGGATGAGGAGAAAATAATGAATGCAAAGGAAGAGAGTGGGTTCA   120
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 GGGAGAGAAGCAGAGGATGAGGAGAAAATAATGAATGTCAAAGGAAGAGAGTGGGTTCA   120

Db    121 ATGCTGCTTGTCTCAACTGTAATGGTTGGTTGTTTTGGGAATACATCAACAGCCCAGAAGGT   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 ATGCTGCTTGTCTCAACTGTAATGGTTGGTTGTTTTGGGAATACATCAACAGCCCAGAAGGT  180

Db    181 TCTTGTTCTTGGATATACCAGCAAAAAAACCCAGAGAAGTTGGGCAGCTGCTCAGAGGGGC   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 TCTTGTTCTTGGATATACCAGCAAAAAAACCCAGAGAAGTTGGGCAGCTGCTCAGAGGGGC   240

Db    241 TGGTGGTTTCCGACCTGGTTTAACAATGGGACTCACAGTTACCACGCGAAGAGAAGACGCT   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 TGGTGGTTTCCGACCTGGTTTAACAATGGGACTCACAGTTACCACGCGAAGAGAAGACGCT   300

Db    301 ATAGGCAACGAAAAAGGAACAAAAGAAGACACACAGGAGGAGGAGCTTCCGCTAGTGGAC   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 ATAGGCAACGAAAAAGGAACAAAAGAAGACACACAGGAGGAGGAGCTTCCGCTAGTGGAC   360
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Db    421 GTATGGGAAGGCAGCACTACAACAGAGCCGTCTTTAGATAATTTATAATGCCAAACAGAAAATT   480
Qy    421 GTATGGGAAGGCAGCACTACAACAGAGCCGTCTTTAGATAATTTA...                   480

Db    481 ACCGTGGGCGTTGACGGTTTTTTCGCTGCCGGAGAGATACATTGAGCATTACTTGGAGGTTC   540
Qy    481 ACCGTGGGCGTTGACGGTTTTTTCGCTGCCGGAGAGATACATTGAGCATTACTTGGAGGTTC   540

Db    541 TTAATATCTGCAAATACATACTTCATGTGTTGGCCACAAAGTCATCTTTACATCATGGTG    600
Qy    541 TTAATATCTGCAAATACATACTTCATGTGTTGGCCACAAAGTCATCTTTACATCATGGTG    600

Db    601 GATGATAATCTCCAGGATGCCTTTGATAGAGCTGGGTTCCTCTGCGTTCCTTTAAAGTGTTT   660
Qy    601 GATGATAATCTCCAGGATCCCTTTGATAGAGCTGGGTCCTCGCGTTCCTTTAAAGTGTTT   660

Db    661 GAGATCAAGTCCGAGAAGAGAGGTGGGCAAGAACAATCAGCATGATGCGCGCATGAAGACCATCGGG   720
Qy    661 GAGATCAAGTCCGAGAAGAGAGGTGGGCAAGAACAATCAGCATGATGCGCGCATGAAGACCATCGGG   720

Db    721 GAGACACATCCTGCCCACAATCCAGCACGAGGTGGAAGACATCACCATGATGCGGCATGAT   780
Qy    721 GAGACACATCCTGCCCACAATCCAGCACGAGGTGGAAGACATCACCATGATGCGGCATGAT   780

Db    781 CAGGTCTTCCAAAACAACTTTGGGGTGGGAAGACCCTGGGGGCCAGTCGGCGGTCGCTACAG   840
Qy    781 CAGGTCTTCCAAAACAACTTTGGGGTGGGAAGACCCTGGGGGCCAGTCGGCGGTCGCTACAG   840

Db    841 GCCTGGGTGGTACAAAGGCACATCCTGACGAGTTCACCTACGGAGGGGGAAGGGAGTCCCGA   900
Qy    841 GCCTGGGTGGTACAAAGGCACATCCTGACGAGTTCACCTACGGAGGGGGAAGGGAGTCCCGA   900

Db    901 GCCTACATTCCGTTGGGCCAGGGGGATTTTTTATTACCACGCAGCCCATTTTTGGGGGAACA   960
Qy    901 GCCTACATTCCGTTGGGCCAGGGGGATTTTTTATTACCACGCAGCCCATTTTTGGGGGAACA   960

Db    961 CCCACTCAGGTTCAAACATCACTCAGAGTGCTTCAAAGGGAATCCTCCAGGACAAGGAA   1020
Qy    961 CCCACTCAGGTTCAAACATCACTCAGAGTGCTTCAAAGGGAATCCTCCAGGACAAGGAA   1020

Db   1021 AATGACATAGAAGCCGAGTGGGCATGATGAGAAAGCCATCTAAACAAGTATATTAATTCTCAAC   1080
Qy   1021 AATGACATAGAACCCGAGTGGGCATGATGAGAAAGCCACCTAAACAAGTATTTCTCTCAAC      1080

Db   1081 AAACCCACTAAAAATCTTATCCCCAGAAATACTGCTCGGATTATCATAAAGGCATGTCTGTG   1140
Qy   1081 AAACCCACTAAAAATCTTATCCCCAGAAATACTGCTCGGATTATCATAAAGGCATGTCTGTG   1140

Db   1141 GATAATTAGGATTGTCAGATAACTTGGCAGAAAAAAGAGTATAAATTGGTTTAGAAATAAC   1200
Qy   1141 GATATTAGGATTGTCAAGATAGCTTGGCAGAAAAAGAGTATAAATTGGTTTAGAAATAAC     1200

Db   1201 ATCTGACTTTAAATTGTCCCAGCCAGTTTTCTGAATTTGAAAGAGTATTTACTCTGGCTACT   1260
Qy   1201 ATCTGACTTTAAATTGTCCCAGCCAGTTTTCTGAATTTGAAAGAGTATTACTCTGGCTACT   1260

Db   1261 TCCTCAGAGAGTAGCACTTAAATTTAACTTTTAAAAAATACTAACAAAATACCAACAC    1320
Qy   1261 TCCTCAGAGAGTAGCACTTAAATTTTAACTTTTAAAAAATACTAACAAAATACCAACAC   1320

Db   1321 AGTAAGTACATATTATTCTTCCTTGCAAACTTTGAGCCTTGTCAAATGGGAGAATGACTCT   1380
Qy   1321 AGTAAGTACAIATTATTCTTCCTTGCAAACTTTGAGCCTTGTCAAATGGGAGAATGACTCT   1380

Db   1381 GTGGTAAATCAGATGTAAATTCCCAGTGATTTC   1412
Qy   1381 GTGGTAAATCAGATGTAAATTCCCAGTGATTTC   1412
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